SEQUENCE LISTING

```
<110> Bermudes, G.
      King, I.
      Clairmont, C.
      Lin, S.
      Belcourt, M.

<120> COMPOSITIONS AND METHODS FOR
      TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES


<130> 8002-059

<150> 60/157,581
<151> 1999-10-04

<150> 60/157,637
<151> 1999-10-04

<160> 61

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<210> 1
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<223> Forward primer

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gaagatcttc cggaggaggg gaaatg                                      26

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<400> 2
cgggatccga gctcgagggc ccgggaaagg atctaagaag atcc                  44

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<213> Homo sapiens

<220>
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<222> (1)...(474)

<400> 3
atg gta cgt agc tcc tct cgc act ccg tcc gat aag ccg gtt gct cat   48
Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
 1               5                  10                  15
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gta gtt gct aac cct cag gca gaa ggt cag ctg cag tgg ctg aac cgt        96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
            20              25              30

cgc gct aac gcc ctg ctg gca aac ggc gtt gag ctc cgt gat aac cag       144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
        35              40              45

ctc gtg gta cct tct gaa ggt ctg tac ctg atc tat tct caa gta ctg       192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
    50              55              60

ttc aag ggt cag ggc tgc ccg tcg act cat gtt ctg ctg act cac acc       240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
65              70              75              80

atc agc cgt att gct gta tct tac cag acc aaa gtt aac ctg ctg agc       288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
            85              90              95

gct atc aag tct ccg tgc cag cgt gaa act ccc gag ggt gca gaa gcg       336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
            100             105             110

aaa cca tgg tat gaa ccg atc tac ctg ggt ggc gta ttt caa ctg gag       384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
        115             120             125

aaa ggt gac cgt ctg tcc gca gaa atc aac cgt cct gac tat cta gat       432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
    130             135             140

ttc gct gaa tct ggc cag gtg tac ttc ggt att atc gca ctg               474
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145             150             155

taa                                                                    477
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<210> 4
<211> 158
<212> PRT
<213> Homo sapiens

<400> 4
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Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
1               5               10              15
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
            20              25              30
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
        35              40              45
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
    50              55              60
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
65              70              75              80
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
            85              90              95
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
            100             105             110
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
        115             120             125
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
    130             135             140
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Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145   150   155

    <210> 5
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    <213> Artificial Sequence

    <220>
    <223> Forward primer

    <400> 5
ccgacgcgtt gacacctgaa aactggag   28

    <210> 6
    <211> 29
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Reverse primer

    <400> 6
ccgacgcgtg aaaggatctc aagaagatc   29

    <210> 7
    <211> 543
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Fusion construct

    <221> CDS
    <222> (1)...(540)

    <400> 7
atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct   48
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1   5   10   15

acc gta gcg cag gcc cat atg gta cgt agc tcc tct cgc act ccg tcc   96
Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
                20   25   30

gat aag ccg gtt gct cat gta gtt gct aac cct cag gca gaa ggt cag   144
Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
            35   40   45

ctg cag tgg ctg aac cgt cgc gct aac gcc ctg ctg gca aac ggc gtt   192
Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
        50   55   60

gag ctc cgt gat aac cag ctc gtg gta cct tct gaa ggt ctg tac ctg   240
Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
65   70   75   80

atc tat tct caa gta ctg ttc aag ggt cag ggc tgc ccg tcg act cat   288
Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
                85   90   95

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gtt ctg ctg act cac acc atc agc cgt att gct gta tct tac cag acc        336
Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
            100             105             110

aaa gtt aac ctg ctg agc gct atc aag tct ccg tgc cag cgt gaa act        384
Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
            115             120             125

ccc gag ggt gca gaa gcg aaa cca tgg tat gaa ccg atc tac ctg ggt        432
Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
        130             135             140

ggc gta ttt caa ctg gag aaa ggt gac cgt ctg tcc gca gaa atc aac        480
Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
145             150             155             160

cgt cct gac tat cta gat ttc gct gaa tct ggc cag gtg tac ttc ggt        528
Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
            165             170             175

att atc gca ctg taa                                                     543
Ile Ile Ala Leu
            180


        <210> 8
        <211> 180
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Fusion construct

        <400> 8
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1               5               10              15
Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
            20              25              30
Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
        35              40              45
Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
    50              55              60
Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
65              70              75              80
Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
                85              90              95
Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
            100             105             110
Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
            115             120             125
Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
        130             135             140
Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
145             150             155             160
Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
            165             170             175
Ile Ile Ala Leu
            180

        <210> 9
        <211> 801
        <212> DNA
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-4-

<213> Artificial Sequence

<220>
<223> Fusion construct

<221> CDS
<222> (1)...(798)

<400> 9
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atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct        48
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1               5                   10                  15

acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac        96
Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
                20                  25                  30

aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt       144
Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
            35                  40                  45

tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa       192
Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
        50                  55                  60

gtc aag tgg caa ctc cgt cag ctc gtt aga aag atg att ttg aga acc       240
Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
65                  70                  75                  80

tct gag gaa acc att tct aca gtt caa gaa aag caa caa aat att tct       288
Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
                85                  90                  95

ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act       336
Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
            100                 105                 110

ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat       384
Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
            115                 120                 125

gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt       432
Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
        130                 135                 140

ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc       480
Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
145                 150                 155                 160

atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga       528
Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
                165                 170                 175

ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc       576
Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
                180                 185                 190

caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg       624
Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
            195                 200                 205
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aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga ctc      672
Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
210                     215                 220

tat tcc atc tat caa ggg gga ata ttt gag ctt aag gaa aat gac aga      720
Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
225                 230                 235                     240

att ttt gtt tct gta aca aat gag cac ttg ata gac atg gac cat gaa      768
Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu
                245                 250                 255

gcc agt ttt ttc ggg gcc ttt tta gtt ggc taa                         801
Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
                260                 265


        <210> 10
        <211> 266
        <212> PRT
        <213> Artificial Sequence

        <220>
        <223> Fusion construct

        <400> 10
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1               5                   10                  15
Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
            20              25                  30
Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
        35                  40                  45
Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
        50                  55                  60
Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
65                  70                  75                  80
Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
            85                  90                  95
Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
            100                 105                 110
Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
        115                 120                 125
Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
        130                 135                 140
Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
145                 150                 155                 160
Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
                165                 170                 175
Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
            180                 185                 190
Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
        195                 200                 205
Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
210                     215                 220
Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
225                 230                 235                     240
Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu
                245                 250                 255
Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
                260                 265
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<210> 11
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion construct

<221> CDS
<222> (1)...(462)

<400> 11

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atg aaa aag acg gct ctg gcg ctt ctg ctc ttg ctg tta gcg ctg act       48
Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Leu Leu Ala Leu Thr
 1               5                   10                  15

agt gta gcg cag gcc gct cct act agc tcg agc act aag aaa act caa       96
Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
                20                  25                  30

ctg caa ttg gag cat ctg ctg ctg gat ctg cag atg att ctg aat ggc      144
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
            35                  40                  45

atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa      192
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
        50                  55                  60

ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg      240
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
 65                  70                  75                  80

gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct      288
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
                85                  90                  95

aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta      336
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
            100                 105                 110

atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac      384
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
        115                 120                 125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc      432
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
 130                 135                 140

ttt gcc caa tcg atc att agc acg tta act taa                          465
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145                 150
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<210> 12
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion construct

<400> 12
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Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Leu Leu Ala Leu Thr
1               5                   10                  15
Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
                20                  25                  30
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
            35                  40                  45
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
    50                  55                  60
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
65                  70                  75                  80
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
                85                  90                  95
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
                100                 105                 110
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
            115                 120                 125
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
    130                 135                 140
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145                 150
```

<210> 13
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion construct

<221> CDS
<222> (1)...(462)

<400> 13
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atg aaa cag tcg act ctg gcg ctt ctg ctc ttg ctg tta gcg ctg act      48
Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Leu Ala Leu Thr
1               5                   10                  15

agt gtg gcc aaa gcg gct cct act agc tcg agc act aag aaa act caa      96
Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
                20                  25                  30

ctg caa ttg gag cat ctg ctg ctg gat ctg cag atg att ctg aat ggc     144
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
            35                  40                  45

atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa     192
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
    50                  55                  60

ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg     240
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
65                  70                  75                  80

gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct     288
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
                85                  90                  95

aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta     336
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
                100                 105                 110
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```
atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac        384
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
        115             120                 125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc        432
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
    130             135                 140

ttt gcc caa tcg atc att agc acg tta act taa                           465
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145                 150
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        <210> 14
        <211> 154
        <212> PRT
        <213> Artificial Sequence

        <220>
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        <400> 14
Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Leu Ala Leu Thr
1               5                   10                  15
Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
            20                  25                  30
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
        35                  40                  45
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
    50                  55                  60
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
65                  70                  75                  80
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
                85                  90                  95
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
            100                 105                 110
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
        115                 120                 125
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
        130                 135                 140
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145                 150
```

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        <210> 15
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        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Forward primer

        <400> 15
agtctagaca atcaggcgaa gaacgg                                           26
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        <210> 16
        <211> 25
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Reverse primer
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    <400> 16
agccatggag tcaccctcac ttttc                                    25

    <210> 17
    <211> 31
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Forward primer

    <400> 17
ggatccttaa gacccacttt cacatttaag t                             31

    <210> 18
    <211> 28
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Reverse primer

    <400> 18
ggttccatgg ttcacttttc tctatcac                                 28

    <210> 19
    <211> 33
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Forward primer

    <400> 19
gtgtccatgg ggcacagcca ccgcgacttc cag                           33

    <210> 20
    <211> 34
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Reverse primer

    <400> 20
acacgagctc ctacttggag gcagtcatga agct                          34

    <210> 21
    <211> 72
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Forward primer

    <400> 21
gtgtccatgg ctcggcgggc aagtgtcggg actgaccatc atcatcatca tcatcacagc   60
caccgcgact tc                                                  72

    <210> 22
    <211> 35
    <212> DNA
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-10-

<210> Artificial Sequence

<220>
<223> Reverse primer

<400> 22
gtgcggatcc ctacttggag gcagtcatga agctg   35

<210> 23
<211> 16
<212> PRT
<213> Homo sapiens

<400> 23
Met Ala Arg Arg Ala Ser Val Gly Thr Asp His His His His His
1   5   10   15

<210> 24
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide sequence TiP 13.40

<400> 24
Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg
1   5   10   15
Val Val Met Tyr Glu Gly
            20

<210> 25
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding TiP13.40

<400> 25
gcgtaccgct ggcgcctgtc ccatcgcccg aaaaccggct ttatccgcgt ggtgatgtac   60
gaaggc   66

<210> 26
<211> 101
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 26
gtgtactagt gtggcgcagg cggcgtaccg ctggcgcctg tcccatcgcc cgaaaaccgg   60
ctttatccgc gtggtgatgt acgaaggcta aggatccgcg c   101

<210> 27
<211> 101
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 27
gcgcggatcc ttagccttcg tacatcacca cgcggataaa gccggttttc gggcgatggg   60
acaggcgcca gcggtacgcc gcctgcgcca cactagtaca c   101

        <210> 28
        <211> 101
        <212> PRT
        <213> Homo sapiens

        <400> 28
Met Ser Ser Ala Ala Gly Phe Cys Ala Ser Arg Pro Gly Leu Leu Phe
1   5   10   15
Leu Gly Leu Leu Leu Leu Pro Leu Val Val Ala Phe Ala Ser Ala Glu
            20   25   30
Ala Glu Glu Asp Gly Asp Leu Gln Cys Leu Cys Val Lys Thr Thr Ser
        35   40   45
Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val Ile Lys Ala Gly
    50   55   60
Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys Asn Gly Arg
65   70   75   80
Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys Lys Ile Ile Lys
                85   90   95
Lys Leu Leu Glu Ser
        100

        <210> 29
        <211> 106
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Oligonucleotide

        <400> 29
cttcactagt gtggcgcagg cgaacggccg caaatctgc ctggacctgc aggcgccgct   60
gtacaaaaaa atcatcaaaa aactgctgga aagctaagga tccgcg   106

        <210> 30
        <211> 106
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Oligonucleotide

        <400> 30
cgcggatcct tagctttcca gcagtttttt gatgattttt ttgtacagcg gcgcctgcag   60
gtccaggcag attttgcggc cgttcgcctg cgccacacta gtgaag   106

        <210> 31
        <211> 85
        <212> PRT
        <213> Homo sapiens

        <400> 31
Ile Tyr Ser Phe Asp Gly Arg Asp Ile Met Thr Asp Pro Ser Trp Pro
1   5   10   15
Gln Lys Val Ile Trp His Gly Ser Ser Pro His Gly Val Arg Leu Val
            20   25   30
Asp Asn Tyr Cys Glu Ala Trp Arg Thr Ala Asp Thr Ala Val Thr Gly
        35   40   45

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Leu Ala Ser Pro Leu Ser Thr Gly Lys Ile Leu Asp Gln Lys Ala Tyr
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65                  70                  75                  80
Thr Asp Ala Arg Lys
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        <212> DNA
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        <220>
        <223> Oligonucleotide

        <400> 32
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        <210> 33
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        <220>
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        <210> 34
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        <213> E. coli

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ctgatttcta aaaaatttttc cacctgaact tgacagaaaa aacgatgacg agtacttttt   180
gatctgtaca taaacccagt ggttttatgt acagtattaa tcgtgtaatc aattgtttta   240
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<210> 35
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 35
gtgtcatgaa aatgggtaac caatggcaac   30

<210> 36
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 36
cacagagctc gcgctaacaa aacagcacaa gggag   35

<210> 37
<211> 37
<212> DNA
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<220>
<223> Forward primer

-15-

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gtgtccatgg ctaaaacatt attaatagct gcatcgc                              37

            <210> 38
            <211> 29
            <212> DNA
            <213> Artificial Sequence

            <220>
            <223> Reverse primer

            <400> 38
gtgtctgcag aactgactga attgagatg                                       29

            <210> 39
            <211> 37
            <212> DNA
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            <220>
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            <400> 39
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            <210> 40
            <211> 30
            <212> DNA
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            <220>
            <223> Reverse primer

            <400> 40
cacaggatcc ttactgaacc gcgatccccg                                      30

            <210> 41
            <211> 40
            <212> DNA
            <213> Artificial Sequence

            <220>
            <223> Forward primer

            <400> 41
gtgtgagctc gatcaaccag caagccgtta accctctgac                           40

            <210> 42
            <211> 67
            <212> DNA
            <213> Artificial Sequence

            <220>
            <223> Reverse primer

            <400> 42
gtgtgcatgc ggggggccat ataggccggg gatttaaatg caaacgtccg ccgaaacgcc     60
gacgcac                                                               67

            <210> 43
            <211> 71
            <212> DNA
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<210> Artificial Sequence

<220>
<223> Forward primer

<400> 43
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catgacatcg c   71

<210> 44
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 44
gtgtctcgag gatatcattc tggcctctga cgttgtg   37

<210> 45
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 45
tttttttccat ggctattatg actgaaatcg ttgcagataa aacgg   45

<210> 46
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 46
tttttttaagc ttcccgggtc agacttcagg tacctcaaag agtgtc   46

<210> 47
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 47
ccgctcgaga tgcacggctc caacaagctc cca   33

<210> 48
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer

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        <400> 48
cgcggatcct taggcactcg ccttgagtgc ctg                                            33

        <210> 49
        <211> 102
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Oligonucleotide

        <400> 49
gatcccatgg cttatggcag aaaaaaacgc cgtcagcgcc gtcgcatgaa cgcgctgcag            60
gaagataccc cgccgggccc gtccaccgtg tttcgcccgc cg                              102

        <210> 50
        <211> 103
        <212> DNA
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        <220>
        <223> Oligonucleotide

        <400> 50
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ccagcgggcg ggaggaggtc ggcgggcgaa acacggtgga cgg                            103

        <210> 51
        <211> 102
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Oligonucleotide

        <400> 51
ggcatcgcgg gcatcaccat caccctgtcc ctgtgcggct gcgcgaacgc gcgcgcgccg          60
accctgcgct ccgcgaccgc ggataactcc gaaaacaccg gc                            102

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        <211> 111
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Oligonucleotide

        <400> 52
gcgatattcg gacggatcgc aggagcgttt tttggacggc ggtttcggct gatcggtgcg          60
cagatccggg acgtttttaa agccggtgtt ttcggagtta tccgcggtcg c                  111

        <210> 53
        <211> 111
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Oligonucleotide

        <400> 53
cctgcgatcc gtccgaatat cgcgtctccg aactgaaaga atccctgatc accaccaccc          60
cgtcccgccc gcgcaccgcc cgccgctgca tccgcctctg aaagcttcat g                  111
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<210> 54
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 54
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<210> 55
<211> 98
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 55
gatcccatgg ctcatcacca tcaccaccat tatggccgca aaaaacgccg tcagcgccgt   60
cgcatgaacg cgctgcagga agataccccg ccgggccc   98

<210> 56
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 56
gatcccatgg ctaaaaagac ggctctggcg cttctgctct tgctgttagc gctgactagt   60
gtagcgcagg cctatggccg caaaaaacgc cgtcagcgcc   100

<210> 57
<211> 551
<212> DNA
<213> Bacteriophage

<220>
<221> CDS
<222> (7)...(408)

<221> modified_base
<222> (1)...(1)
<223> n=a, c, g, or t

<400> 57
nagacc atg gct tat ggc aga aaa aaa aga aga cag aga aga aga atg   48
       Met Ala Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Met
       1   5   10

aac gcg ctg cag gaa gat acc ccg ccg ggc ccg tcc acc gtg ttt cgc   96
Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly Pro Ser Thr Val Phe Arg
 15   20   25   30

ccg ccg acc tcc tcc cgc ccg ctg gaa acc ccg cat tgc cgc gaa atc   144
Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile
                35   40   45

cgc atc ggc atc gcg ggc atc acc atc acc ctg tcc ctg tgc ggc tgc   192

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Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys
            50                  55              60

gcg aac gcg cgc gcg ccg acc ctg cgc tcc gcg acc gcg gat aac tcc    240
Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser
            65                  70              75

gaa aac acc ggc ttt aaa aac gtc ccg gat ctg cgc acc gat cag ccg    288
Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro
    80                  85                  90

aaa ccg ccg tcc aaa aaa cgc tcc tgc gat ccg tcc gaa tat cgc gtc    336
Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val
    95                  100                 105                 110

tcc gaa ctg aaa gaa tcc ctg atc acc acc acc ccg tcc cgc ccg cgc    384
Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro Ser Arg Pro Arg
                115                 120                 125

acc gcc cgc cgc tgc atc cgc ctc tgaaagcttg gctgttttgg cggatgagag    438
Thr Ala Arg Arg Cys Ile Arg Leu
                130

aagattttca gcctgataca gattaaatca gaacgcagaa gcggtctgat aaaacagaat    498
ttgcctggcg gcagtagcgc ggtggtccca cctgacccca tgccgaactc aga           551
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        <210> 58
        <211> 134
        <212> PRT
        <213> Bacteriophage

        <400> 58
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1                 5                   10                  15
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                20                  25                  30
Thr Ser Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile Arg Ile
            35                  40                  45
Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys Ala Asn
    50                  55                  60
Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser Glu Asn
65                  70                  75                  80
Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro Lys Pro
                85                  90                  95
Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val Ser Glu
            100                 105                 110
Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro Ser Arg Pro Arg Thr Ala
    115                 120                 125
Arg Arg Cys Ile Arg Leu
    130
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        <210> 59
        <211> 444
        <212> DNA
        <213> Bacteriophage

        <220>
        <221> modified_base
        <222> (1)...(1)
        <223> n=a, c, g, or t

        <221> CDS

<222> (7)...(427)

<400> 59
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       Met Ala His His His His His His Tyr Gly Arg Lys Lys Arg
       1               5                   10

cgt cag cgc cgt cgc atg aac gcg ctg cag gaa gat acc ccg ccg ggc       96
Arg Gln Arg Arg Arg Met Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly
15              20              25                  30

ccg tcc acc gtg ttt cgc ccg ccg acc tcc tcc cgc ccg ctg gaa acc      144
Pro Ser Thr Val Phe Arg Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr
                35              40                  45

ccg cat tgc cgc gaa atc cgc atc ggc atc gcg ggc atc acc atc acc      192
Pro His Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr
            50                  55                  60

ctg tcc ctg tgc ggc tgc gcg aac gcg cgc gcg ccg acc ctg cgc tcc      240
Leu Ser Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser
        65                  70                  75

gcg acc gcg gat aac tcc gaa aac acc ggc ttt aaa aac gtc ccg gat      288
Ala Thr Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp
    80                  85                  90

ctg cgc acc gat cag ccg aaa ccg ccg tcc aaa aaa cgc tcc tgc gat      336
Leu Arg Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp
95                  100                 105                 110

ccg tcc gaa tat cgc gtc tcc gaa ctg aaa gaa tcc ctg atc acc acc      384
Pro Ser Glu Tyr Arg Val Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr
                115                 120                 125

acc ccg tcc cgc ccg cgc acc gcc cgc cgc tgc atc cgc ctc t           427
Thr Pro Ser Arg Pro Arg Thr Ala Arg Arg Cys Ile Arg Leu
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gaaagcttgg ctgtttt                                                   444
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<210> 60
<211> 140
<212> PRT
<213> Bacteriophage

<400> 60
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Arg Arg Arg Met Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly Pro Ser
            20              25                  30
Thr Val Phe Arg Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr Pro His
        35                  40                  45
Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser
    50                  55                  60
Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr
65                  70                  75                  80
Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg
                85                  90                  95
Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser
            100                 105                 110
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Glu Tyr Arg Val Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro
        115                 120                 125
Ser Arg Pro Arg Thr Ala Arg Arg Cys Ile Arg Leu
    130                 135                 140


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    <211> 1565
    <212> DNA
    <213> Salmonella

    <400> 61
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    ggcgatccgg agctggttgg tatccagaaa gcgctgattc gccgtgcgcg tcagctaaac   120
    cgcgcagtca tcaccgcaac gcaaatgatg gagtcgatga tcaccaaccc gatgccgacc   180
    cgtgcggaag tgatggacgt ggcgaacgcc gtcctggatg gcacggatgc ggttatgctg   240
    tctgccgaaa ccgcagccgg tcagtatcct tctgaaaccg ttgccgcaat ggcgcgcgtc   300
    tgcctgggcg cagaaaaaat ccccagcatc aatgtgtcta aacaccgtct cgacgtgcag   360
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    gccatcatcg ccattgcctg tggcgcggtg gcgaacatct catcgacaat cgcttcgcgc   1080
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    accccgtcag accttccgtg cgcggcaatt ttgctgtcag agggttaacg gcttgctggt   1560
    tgatc                                                              1565
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